M

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins

(iii) NUMBER OF SEQUENCES: 108

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SESTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1 Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
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- (viii) ATTORNEY/AGENT INFORMATION:

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 - (d) REFERENCE/DOCKET NUMBER: FJN-060
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 248-7000
 - (B) TELEFAX: (617) 248-7100
- (2) INFORMATION FOR SEQ ID NO:1:
 - SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid

- DEONESS: (D) ToroLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..14
 - (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys 1 5

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid

 - (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..12
 - (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein) "
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys 5 1

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 amino acids

- (B) E:www ino acid (C) ANL_DNESS: (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "(OCIF protein without signal peptide)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 - Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His

 1 10 15
 - Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
 - Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr 35 40 45
 - Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro 50 60
 - Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His 65 70 75 80
 - Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe
 85 90 95
 - Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala
 - Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe 115 120 125
 - Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn 130 135 140
 - Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His 145 150 155 160
 - Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile 165 170 175
 - Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr 180 185 190
 - Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly 195 200 205
 - Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser 210 215 220
 - Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn 225 230 235 240
 - Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys 245 250 255
 - Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu 260 265 270
 - Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala



Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile 290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr 305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe 325 330 335

Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His 340 345 350

Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile 355 360 365

Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "(OCIF protein)"
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (D) OTHER INFORMATION: /note= "(signal peptide)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp 5

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105

in Ala Gly Thr Pro Glu Arg Asn T Al Cys Lys Arg 115 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 230 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly 275 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn 310 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr 340 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 355 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys 365

Leu 380

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420 GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT 480 AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA 540 CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC 600 CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT 660 AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA 720 AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA 780 AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC 840 GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA 900 AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA 960 CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC 1020 ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT 1080

(2) INFORMATION FOR SEO ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

TTATAA

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "(a N-terminal amino acid sequence of the protein)"

GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG

TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC

1140

1200

1206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGTGC	AATCGCACCC	ACAACCGCGT	GTGCGAATGC	300
AAGGAAGGGC	GCTACCTTGA	GATAGAGTTC	TGCTTGAAAC	ATAGGAGCTG	CCCTCCTGGA	360
TTTGGAGTGG	TGCAAGCTGG	AACCCCAGAG	CGAAATACAG	TTTGCAAAAG	ATGTCCAGAT	420
GGGTTCTTCT	CAAATGAGAC	GTCATCTAAA	GCACCCTGTA	GAAAACACAC	AAATTGCAGT	480
GTCTTTGGTC	TCCTGCTAAC	TCAGAAAGGA	AATGCAACAC	ACGACAACAT	ATGTTCCGGA	540
AACAGTGAAT	CAACTCAAAA	ATGTGGAATA	GATGTTACCC	TGTGTGAGGA	GGCATTCTTC	600
AGGTTTGCTG	TTCCTACAAA	GTTTACGCCT	AACTGGCTTA	GTGTCTTGGT	AGACAATTTG	660
CCTGGCACCA	AAGTAAACGC	AGAGAGTGTA	GAGAGGATAA	AACGGCAACA	CAGCTCACAA	720
GAACAGACTT	TCCAGCTGCT	GAAGTTATGG	AAACATCAAA	ACAAAGACCA	AGATATAGTC	780
AAGAAGATCA	TCCAAGATAT	TGACCTCTGT	GAAAACAGCG	TGCAGCGGCA	CATTGGACAT	840
GCTAACCTCA	CCTTCGAGCA	GCTTCGTAGC	TTGATGGAAA	GCTTACCGGG	AAAGAAAGTG	900
GGAGCAGAAG	ACATTGAAAA	AACAATAAAG	GCATGCAAAC	CCAGTGACCA	GATCCTGAAG	960
CTGCTCAGTT	TGTGGCGAAT	AAAAAATGGC	GACCAAGACA	CCTTGAAGGG	CCTAATGCAC	1020
GCACTAAAGC	ACTCAAAGAC	GTACCACTTT	CCCAAAACTG	TCACTCAGAG	TCTAAAGAAG	1080
ACCATCAGGT	TCCTTCACAG	CTTCACAATG	TACAAATTGT	ATCAGAAGTT	ATTTTTAGAA	1140
ATGATAGGTA	ACCAGGTCCA	ATCAGTAAAA	ATAAGCTGCT	TATAA		1185

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 amino acids
 (B) TYPE: amino acid

 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..373

(D) OTHER INFORMATION: /note= "(OCIF2)"

(ix) FEATURE:

(A) NAME/KEY: Peptide (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp -5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys Asn Arg Thr His Asn Arg 60 65 70 75

Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu 80 85 90

Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr 95 100 105

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser 110 115 120

Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser 125 130 135

Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn 140 155 150 155

Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val 160 165 170

Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe 175 180 185

Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys
190 195 200

Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln 205 210 215

Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp 220 225 230 235

Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn 240 245 250

Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu

265

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Arg	Ser	Leu 270	Met	Glu	Ser	Leu	Pro 275	Gly	Lys	Lys	Val	Gly 280	Ala	Glu	Asp
Ile	Glu 285	Lys	Thr	Ile	Lys	Ala 290	Cys	Lys	Pro	Ser	Asp 295	Gln	Ile	Leu	Lys
Leu 300	Leu	Ser	Leu	Trp	Arg 305	Ile	Lys	Asn	Gly	Asp 310	Gln	Asp	Thr	Leu	Lys 315
Gly	Leu	Met	His	Ala 320	Leu	Lys	His	Ser	Lys 325	Thr	Tyr	His	Phe	Pro 330	Lys
Thr	Val	Thr	Gln 335	Ser	Leu	Lys	Lys	Thr 340	Ile	Arg	Phe	Leu	His 345	Ser	Phe
Thr	Met	Tyr: 350	Lys	Leu	Tyr	Gln	Lys 355	Leu	Phe	Leu	Glu	Met 360	Ile	Gly	Asn
	-		_	-	_		_	_	_						

Gln Val Gln Ser Val Lys Ile Ser Cys Leu 365

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1089 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: /note= "(OCIF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAACAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780

AACAAAGACC	T-JAT	CAAGAAGATC	ATCCAAGATA	TTGAC	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	AGTTTGTGGC	GAATAAAAA	TGGCGACCAA	900
GACACCTTGA	AGGGCCTAAT	GCACGCACTA	AAGCACTCAA	AGACGTACCA	CTTTCCCAAA	960
ACTGTCACTC	AGAGTCTAAA	GAAGACCATC	AGGTTCCTTC	ACAGCTTCAC	AATGTACAAA	1020
TTGTATCAGA	AGTTATTTTT	AGAAATGATA	GGTAACCAGG	TCCAATCAGT	AAAAATAAGC	1080
TGCTTATAA						1089

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..341
 - (D) OTHER INFORMATION: /note= "(OCIF3)"
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 - Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 - Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 - Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 - Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 - Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 - Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 - Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 - Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 - Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 - Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 - Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Thr Gln Lys 150 145

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Asn	Al		His 160	Asp	Asn	Ile	Cys	Ser 165	Gly	Ası	F	Glu	Ser 170	Thr
Lys	Cys	Gly 175	Ile	Asp	Val	Thr	Leu 180	Cys	Glu	Glu	Ala	Phe 185	Phe	Arg
Ala	Val 190	Pro	Thr	Lys	Phe	Thr 195	Pro	Asn	Trp	Leu	Ser 200	Val	Leu	Val
Asn 205	Leu	Pro	Gly	Thr	Lys 210	Val	Asn	Ala	Glu	Ser 215	Val	Glu	Arg	Ile
_	Gln	His	Ser	Ser 225	Gln	Glu	Gln	Thr	Phe 230	Gln	Leu	Leu	Lys	Leu 235
Lys	His	Gln	Asn 240	Lys	Asp	Gln	Asp	Ile 245	Val	Lys	Lys	Ile	Ile 250	Gln
Ile	Asp	Leu 255	Cys	Glu	Asn	Ser	Val 260	Gln	Arg	His	Ile	Gly 265	His	Ala
Leu	Ser 270	Leu	Trp	Arg	Île	Lys 275	Asn	Gly	Asp	Gln	Asp 280	Thr	Leu	Lys
Leu 285	Met	His	Ala	Leu	Lys 290	His	Ser	Lys	Thr	Tyr 295	His	Phe	Pro	Lys
	Thr	Gln	Ser	Leu 305	Lys	Lys	Thr	Ile	Arg 310	Phe	Leu	His	Ser	Phe 315
Met	Tyr	Lys	Leu 320	Tyr	Gln	Lys	Leu	Phe 325	Leu	Glu	Met	Ile	Gly 330	Asn
Val	Gln	Ser 335	Val	Lys	Ile	Ser	Cys 340	Leu						
	Lys Ala Asn 205 Arg Lys Lys Leu 285 Val	Ala Val 190 Asn Leu 205 Arg Gln Lys His Ile Asp Leu Ser 270 Leu Met 285 Val Thr	Lys Cys Gly 175 Ala Val Pro 190 Asn Leu Pro 205 Arg Gln His Gln Lys His Gln Leu Ser Leu 270 Leu Met His 285 Val Thr Gln Met Tyr Lys Val Gln Ser	Lys Cys Gly Ile 175 Ala Val Pro Thr 190 Asn Leu Pro Gly 205 Arg Gln His Ser Lys His Gln Asn 240 Ile Asp Leu Cys 255 Leu Ser Leu Trp 270 Leu Met His Ala 285 Val Thr Gln Ser Met Tyr Lys Leu 320 Val Gln Ser Val	Lys Cys Gly Ile Asp 175 Ala Val Pro Thr Lys 190 Asn Leu Pro Gly Thr 205 Arg Gln His Ser Ser 225 Lys His Gln Asn Lys 240 Ile Asp Leu Cys Glu 255 Leu Ser Leu Trp Arg 270 Leu Met His Ala Leu 285 Val Thr Gln Ser Leu 305 Met Tyr Lys Leu Tyr 320 Val Gln Ser Val Lys	Lys Cys Gly Ile Asp Val 175 Ala Val Pro Thr Lys Phe 190 Asn Leu Pro Gly Thr Lys 210 Arg Gln His Ser Ser Gln 225 Lys His Gln Asn Lys Asp 240 Ile Asp Leu Cys Glu Asn 255 Leu Ser Leu Trp Arg Ile 270 Leu Met His Ala Leu Lys 290 Val Thr Gln Ser Leu Lys 305 Met Tyr Lys Leu Tyr Gln 320 Val Gln Ser Val Lys Ile	Lys Cys Gly Ile Asp Val Thr 175 Ala Val Pro Thr Lys Phe Thr 195 Asn Leu Pro Gly Thr Lys Val 210 Arg Gln His Ser Ser Gln Glu 225 Lys His Gln Asn Lys Asp Gln 240 Ile Asp Leu Cys Glu Asn Ser 255 Leu Ser Leu Trp Arg Ile Lys 275 Leu Met His Ala Leu Lys His 285 Val Thr Gln Ser Leu Lys Lys 305 Met Tyr Lys Leu Tyr Gln Lys 100 Val Gln Ser Val Lys Ile Ser	Lys Cys Gly Ile Asp Val Thr Leu 180 Ala Val Pro Thr Lys Phe Thr Pro 195 Asn Leu Pro Gly Thr Lys Val Asn 205 Arg Gln His Ser Ser Gln Glu Gln 225 Lys His Gln Asn Lys Asp Gln Asp 240 Ile Asp Leu Cys Glu Asn Ser Val 255 Leu Ser Leu Trp Arg Ile Lys Asn 270 Leu Met His Ala Leu Lys His Ser 285 Val Thr Gln Ser Leu Lys Lys Thr 305 Met Tyr Lys Leu Tyr Gln Lys Leu Val Gln Ser Val Lys Ile Ser Cys	Lys Cys Gly 11e Asp Val Thr Leu Cys 175 Ala Val Pro Thr Lys Phe Thr Pro Asn 195 Asn Leu Pro Gly Thr Lys Val Asn Ala 205 Arg Gln His Ser Ser Gln Glu Gln Thr 225 Lys His Gln Asn Lys Asp Gln Asp Ile 245 Ile Asp Leu Cys Glu Asn Ser Val Gln 260 Leu Ser Leu Trp Arg Ile Lys Asn Gly 275 Leu Met His Ala Leu Lys His Ser Lys 285 Val Thr Gln Ser Leu Lys Lys Thr Ile 305 Met Tyr Lys Leu Tyr Gln Lys Leu Phe 3225 Val Gln Ser Val Lys Ile Ser Cys Leu	Lys Cys Gly 11e Asp Val Thr Leu Cys Glu 175 Thr Lys Phe Thr Pro Asn Trp 195 Asn Leu 205 Thr Ser Ser Gln Glu Gln Thr Phe 230 Lys His Gln Asn Lys Asp Gln Asp 11e Val 255 Cys Glu Asn Ser Val Gln Arg 270 Thr Arg 11e Lys Asn Gly Asp 275 Thr Ser Leu 285 Thr Gln Ser Leu Lys His Ser Lys Thr 285 Thr Ser Lys Thr Ser Lys Thr Lys Lys Lys Thr Lys Leu Tyr Gln Lys Leu Phe Leu 320 Val Gln Ser Val Gln Ser Cys Leu Cys Leu Cys Leu Cys Leu Cys Leu Cys His Ser Lys Thr Ser Lys Thr Ser Lys Thr Ser Cys Leu Cys Lys Cys Leu Cys Cys Leu Cys Leu Cys Cys Cys Leu Cys	Lys Cys Gly 11e Asp Val Thr Leu Cys Glu Glu 175 Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu 195 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser 205 Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln 230 Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys 245 Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His 255 Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln 270 Leu Met His Ala Leu Lys His Ser Lys Thr Tyr 295 Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe 310 Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu 325 Val Gln Ser Val Lys Ile Ser Cys Leu	Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala 180 Ala Val Pro Thr Lys Phe Thr 195 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser 200 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val 205 Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu 230 Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys 245 Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile 255 Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp 280 Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His 285 Val Thr Gln Ser Leu Tyr Gln Lys Leu Phe Leu Glu Met 320 Val Gln Ser Val Lys Ile Ser Cys Leu	Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe 185 Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val 190 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu 205 Arg Gln His Ser Ser Gln Glu Gln Thr Phe 215 Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile 116 Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly 265 Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr 270 Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe 285 Val Thr Gln Ser Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile 320 Val Gln Ser Val Lys Ile Ser Cys Leu	Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe 175 Ala Val Pro Thr Lys Phe Thr 195 Pro Asn Trp Leu Ser Val Leu 200 Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg 215 Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys 230 Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile 250 Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His 265 Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu 280 Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro 285 Val Thr Gln Ser Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly 330 Val Gln Ser Val Lys Ile Ser Cys Leu

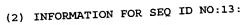
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- (i) SEQUENCE CHARACTERISTICS:

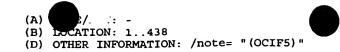
 - (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..465
 - (D) OTHER INFORMATION: /note= "(OCIF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAACAAGT	TGCTGTGCTG	CTCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GTACGTGTCA	ATGTGCAGCA	420



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: /note= "(OCIF4)"
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
- Met Asn Lys Leu Leu Cys Cys Ser Leu Val Phe Leu Asp Ile Ser Ile
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
- Gly Val Val Gln Ala Gly Thr Cys Gln Cys Ala Ala Lys Leu Ile Arg
- Ile Met Gln Ser Gln Ile Val Val Thr Val
- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAACAAGT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GATGCAGGAG	AAGACCCAAG	420
CCACAGATAT	GTATCTGA					438

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: /note= "(OCIF5)"
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
- Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 50
 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe

Today was not taken



Gly Val Val Gln Ala Gly Cys Arg Arg Pro Lys Pro Gln Ile Cys 110 115 120

Ile

(2)	INFORMATION	FOR	SEQ	ID	NO:16:
-----	-------------	-----	-----	----	--------

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

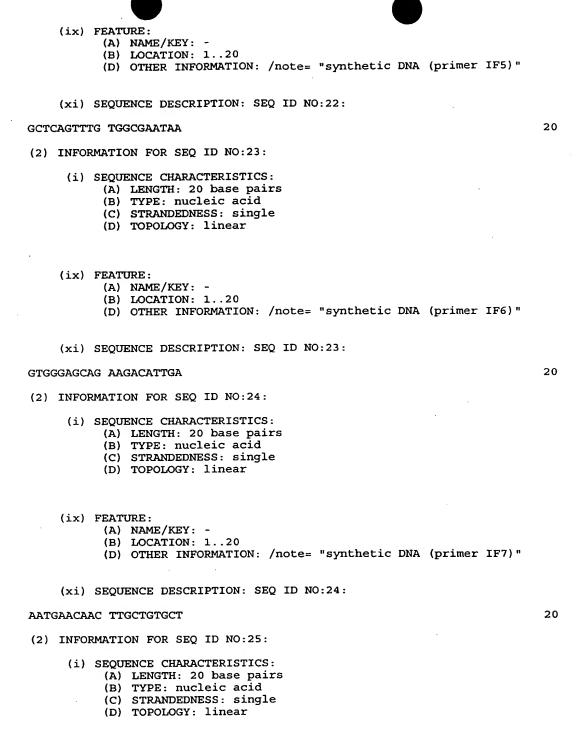
(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2)	INFO	RMATI OR SEQ ID NO:19:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ix)	FEATURE: (A) NAME/KEY: - (B) LOCATION: 120 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:	
TCT	rggtc:	TT TGTTTTGATG	20
(2)	INFO	RMATION FOR SEQ ID NO:20:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ix)	FEATURE: (A) NAME/KEY: - (B) LOCATION: 120 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TTA	rtcgc	CA CAAACTGAGC	20
(2)	INFO	RMATION FOR SEQ ID NO:21:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ix)	FEATURE: (A) NAME/KEY: - (B) LOCATION: 120 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:21:	
TTG:	rgaag(CT GTGAAGGAAC	20
(2)	INFO	RMATION FOR SEQ ID NO:22:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	



- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

DESCRIPTION: SEQ ID NO:25: TGACAAATGT CCTCCTGGTA 20 (2) INFORMATION FOR SEQ ID NO:26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..20 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: AGGTAGGTAC CAGGAGGACA 20 (2) INFORMATION FOR SEQ ID NO:27: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..20 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: GAGCTGCCCT CCTGGATTTG 20 (2) INFORMATION FOR SEQ ID NO:28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..20 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAACTGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i)	SEQUE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ix) IF12)"	FEATURE: (A) NAME/KEY: - (B) LOCATION: 120 (D) OTHER INFORMATION: /note= "synthetic DNA (primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GTGTGAGG	AG GCATTCTTCA	20
(2) INFOR	RMATION FOR SEQ ID NO:30:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ix)	FEATURE: (A) NAME/KEY: - (B) LOCATION: 132 (D) OTHER INFORMATION: /note= "synthetic DNA (primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GAATCAACT	C AAAAAAGTGG AATAGATGTT AC	32
(2) INFOR	RMATION FOR SEQ ID NO:31:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ix) C19SR)"	FEATURE: (A) NAME/KEY: - (B) LOCATION: 132 (D) OTHER INFORMATION: /note= "synthetic DNA (primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:31:	
	TA TTCCACTTTT TTGAGTTGAT TC	32
(2) INFOR	RMATION FOR SEQ ID NO:32:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

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(ix) FEATURE:
          (A) NAME/KEY: -
          (D) OTHER INFORMATION: /note= "synthetic DNA (primer
 C20SF) "
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
                                                                            30
ATAGATGTTA CCCTGAGTGA GGAGGCATTC
(2) INFORMATION FOR SEQ ID NO:33:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
     (ix) FEATURE:
            (A) NAME/KEY: -
            (D) OTHER INFORMATION: /note= "synthetic DNA (primer
   C20SR) "
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
                                                                              30
 GAATGCCTCC TCACTCAGGG TAACATCTAT
  (2) INFORMATION FOR SEQ ID NO:34:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 31 base pairs
             (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
       (ix) FEATURE:
              (A) NAME/KEY: -
              (D) OTHER INFORMATION: /note= "synthetic DNA (primer
     C21SF)"
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
                                                                                31
   CAAGATATTG ACCTCAGTGA AAACAGCGTG C
    (2) INFORMATION FOR SEQ ID NO:35:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 31 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
```

19

(D) TOPOLOGY: linear

(A) NAME/KEY: -

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "synthetic A (primer C21SR)"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
GCACGCTGTT TTCACTGAGG GCAATATCTT G	3:
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 131 (D) OTHER INFORMATION: /note= "synthetic DNA (primer C22SF)"</pre>	
•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
AAAACAATAA AGGCAAGCAA ACCCAGTGAC C	31
(2) INFORMATION FOR SEQ ID NO:37:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 131 (D) OTHER INFORMATION: /note= "synthetic DNA (primer C22SR)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GGTCACTGGG TTTGCTTGCC TTTATTGTTT T	31
(2) INFORMATION FOR SEQ ID NO:38:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 131 (D) OTHER INFORMATION: /note= "synthetic DNA (primer C23SF)"</pre>	

DESCRIPTION: SEQ ID NO:38: TCAGTAAAAA TAAGCAGCTT ATAACTGGCC A 31 (2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..31 (D) OTHER INFORMATION: /note= "synthetic DNA (primer C23SR) " (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39: TGGCCAGTTA TAAGCTGCTT ATTTTTACTG A 31 (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..22 (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF14)" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: TTGGGGTTTA TTGGAGGAGA TG 22 (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: -(B) LOCATION: 1..36 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1F) " (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

36

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENC CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	,
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 136 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1R)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GTCAGGGCAA GGTTCCTGGG TGGTCCACTT AATGGA	36
(2) INFORMATION FOR SEQ ID NO:43:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	2.5
ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT	36
(2) INFORMATION FOR SEQ ID NO:44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 136 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR2R)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
TTCCTTGCAT TCGGCGCACA CGGTCTTCCA CTTTGC	36
(2) INFORMATION FOR SEQ ID NO:45:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

CHARACTERISTICS:

(D) POLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 136 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR3F)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA	36
(2) INFORMATION FOR SEQ ID NO:46:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
ATCTGGACAT CTGCACACGC GGTTGTGGGT GCGATT	36
(2) INFORMATION FOR SEQ ID NO:47:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 136 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4F)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
ACAGTTTGCA AATCCGGAAA CAGTGAATCA ACTCAA	36

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ix) FEATURE:

(B) (D) DCR4R) "	DOCATION: 136 OTHER INFORMATION: /note= "synthetic DNA (primer	
	•	
(xi) SEQUE	ENCE DESCRIPTION: SEQ ID NO:48:	
ACTGTTTCCG GAT	TTTGCAAA CTGTATTTCG CTCTGG	36
(2) INFORMATIO	ON FOR SEQ ID NO:49:	
(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 36 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(B)	URE: NAME/KEY: - LOCATION: 136 OTHER INFORMATION: /note= "synthetic DNA (primer	
(xi) SEQUE	ENCE DESCRIPTION: SEQ ID NO:49:	
AATGTGGAAT AGA	ATATTGAC CTCTGTGAAA ACAGCG	36
(2) INFORMATIO	ON FOR SEQ ID NO:50:	
(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 36 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(B)	URE: NAME/KEY: - LOCATION: 136 OTHER INFORMATION: /note= "synthetic DNA (primer	
(xi) SEQUE	ENCE DESCRIPTION: SEQ ID NO:50:	
AGAGGTCAAT ATC	CTATTCCA CATTTTGAG TTGATT	36
(2) INFORMATIO	ON FOR SEQ ID NO:51:	
(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 36 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(dec) proper	THE.	

- DDD2F)"

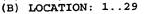
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT	36
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 136 (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2R)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GCTTTAGTGC GTCTTGGATG ATCTTCTTGA CTATAT	36
(2) INFORMATION FOR SEQ ID NO:53:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 129 (D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoIF)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
GGCTCGAGCG CCCAGCCGCC GCCTCCAAG	29
(2) INFORMATION FOR SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
TTTGAGTGCT TTAGTGCGTG	20
III.G.G.G.G. III.G.G.G.G.	~ ~

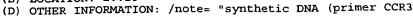
DR SGQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 130 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CLF)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
TCAGTAAAAA TAAGCTAACT GGAAATGGCC	30
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 130 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CL R)"</pre>	
(with appropriate programmers), and ID NO. E.C.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56: GGCCATTTCC AGTTAGCTTA TTTTTACTGA	30
(2) INFORMATION FOR SEQ ID NO:57:	30
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 129 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CC R)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
CCGGATCCTC AGTGCTTTAG TGCGTGCAT	25
(2) INFORMATION FOR SEQ ID NO:58:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 29 base pairs(B) TYPE: nucleic acid	

		•	
R)		FEATURE: (A) NAME/KEY: - (B) LOCATION: 129 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:58:	
CCGC	SATCC	IC ATTGGATGAT CTTCTTGAC	29
(2)	2) INFORMATION FOR SEQ ID NO:59:		
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
R)		FEATURE: (A) NAME/KEY: - (B) LOCATION: 129 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:59:	
CCGC	SATCC'	IC ATATTCCACA TTTTTGAGT	29
(2)	(2) INFORMATION FOR SEQ ID NO:60:		
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
R)		FEATURE: (A) NAME/KEY: - (B) LOCATION: 129 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4)	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:60:	
CCGC	CCGGATCCTC ATTTGCAAAC TGTATTTCG		29
(2) INFORMATION FOR SEQ ID NO:61:			
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

ANDEUWESS: single SPOLOGY: linear

- (ix) FEATU
 - (A) N. Æ/KEY: -





29

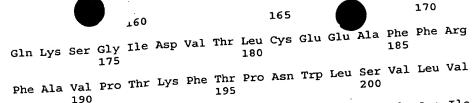
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCGGATCCTC ATTCGCACAC GCGGTTGTG

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "OCIF-C19S"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120
- Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135
- Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 145 150 155
- Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr



Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 225

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln 220

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr 335

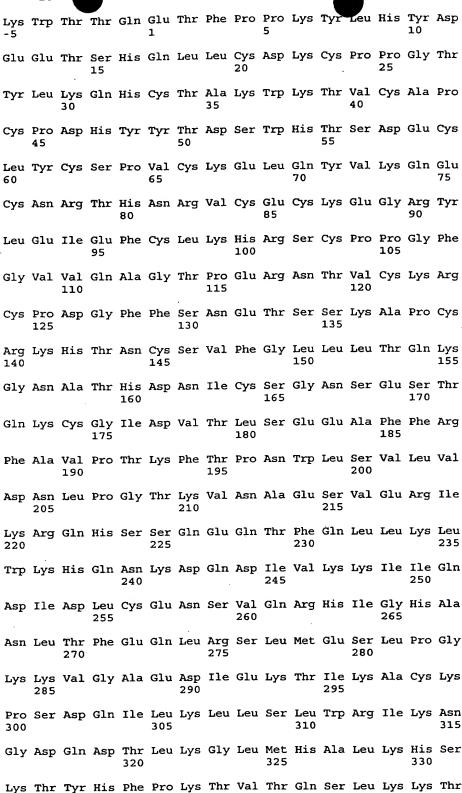
Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys

Leu 380

- (2) INFORMATION FOR SEQ ID NO:63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "OCIF-C20S"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile



His Ser Phe Thr Met Tyr Lys Leu Gln Lys Leu Ile Arg Phe

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys 370

Leu 380

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid (C) STRANDEDNESS:

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "OCIF-C21S"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
- Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 130
- Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
- Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 160

The Asp Val Thr Leu Cys Glu Gly a Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln 245 Asp Ile Asp Leu Ser Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys 290 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn 300 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 325 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr 340 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 350 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys 365 370 375

Leu 380

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "OCIF-C22S"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Th. Gln Glu Thr Phe Pro Pro Lys en Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 100 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 165 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val 195 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 225 220 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln 245 240 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 325 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu

355

Phe Leu Glamet Ile Gly Asn Gln Val Gln Ser Van ys Ile Ser Cys

Leu 380

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..380
 - (D) OTHER INFORMATION: /note= "OCIF-C23S"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 50 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
- Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135
- Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 145 150 150
- Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 160 165 170
- Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg 175 180 185

Phe Ala V Pro fhr Lys Phe Thr Pro Asn Trp L er Val Leu Val

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly 270 275 280

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn 300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr 335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 350 355 360

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Ser 365 370 375

Leu

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..339
 - (D) OTHER INFORMATION: /note= "OCIF-DCR1"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser -5 1 10 . • • . •

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Ser Asp Glu Cys Leu Tyr Cys Ser Hard /al Cys Lys Glu Trp His ' Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu 70 Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn 160 165 Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln 180 Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu 260 Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met 305 310 Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val 320

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

Gln Ser Val Lys Ile Ser Cys Leu 335

(A) LENGTH: 359 amino acids

- (B) TamaMino acid (C) Shandbuness:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..338
 - (D) OTHER INFORMATION: /note= "OCIF-DCR2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Glu 30 35 40
- Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg 45 50 55
- Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg
 60 65 70 75
- Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr 80 90
- Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly 95 100 105
- Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser 110 115 120
- Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys
- Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn 140 145 150 150
- Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala
 160 165 170
- Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr
- Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile 190 195 200
- Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln
- Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu 220 225 230 235
- Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys

Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Ser

Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met 270 275 280

His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr 285 290 295

Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr 300 305 310 315

Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln 320 325 330

Ser Val Lys Ile Ser Cys Leu 335

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..342
 - (D) OTHER INFORMATION: /note= "OCIF-DCR3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro $30 \hspace{1cm} 35 \hspace{1cm} 40 \hspace{1cm}$
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 50 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Arg Cys Pro Asp Gly Phe Phe 80 85 90
- Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys 95 100 105
- Ser Val Phe Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp



Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp 125 130

Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys 140 145 150 150

Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr 160 165 170

Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser 175 180 185

Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys 190 195 200

Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu 205 215

Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln 220 225 230 235

Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu 240 245 250

Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu 255 260 265

Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu 270 275 280

Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro 285 290 295

Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser 300 305 310 315

Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly 320 325 330

Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu 335 340

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..338
 - (D) OTHER INFORMATION: /note= "OCIF-DCR4"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Ser 115 Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn 150 Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys 240 Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr 310 Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln 320 325

Ser Val Lys Ile Ser Cys Leu · 335

(2) INFORMATION OR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..305
 - (D) OTHER INFORMATION: /note= "OCIF-DDD1"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro $30 \hspace{1cm} 35 \hspace{1cm} 40 \hspace{1cm}$
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 50 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120
- Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135
- Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 145 150 150
- Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
- Gln Lys Cys Gly Ile Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg 175 180 185
- His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met 190 $$195\$
- Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr 205 210 215

Ile Lys Al Lys Pro Ser Asp Gln Ile Leu Ly Ly Leu Ser Leu 220 235

Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His 240 245 250

Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln 255 260 265

Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys 270 275 280

Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser 285 290 295

Val Lys Ile Ser Cys Leu 300 305

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..306
 - (D) OTHER INFORMATION: /note= "OCIF-DDD2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp -5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120

Cys Pro Asp Phe Phe Ser Asn Glu Thr Ser Ser 135 Ala Pro Cys 135 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 155 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 170 The Asp 175 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val 190 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile 205 Trp Lys His Gln Asn Lys Asp Gln Asp Asp Asp Ala Leu Lys His Ser Ser Gln Glu Gln Thr Phe Gln Lys Lys Lys Ile Ile Gln 235 Trp Lys His Gln Asn Lys Asp Gln Asp 126 Yal Lys Lys Ile Ile Gln 255 Gln Ser Leu Lys Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr 265 Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr 285 Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Lys Gln Leu Tyr Gln Lys Leu 290 Trp Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Lys Tyr Gln Lys Leu 290 Trp Leu His Ser Rhe Gln Val Gln Ser Leu Tyr Gln Lys Leu 290 Trp Leu Glu Met Ile Gly Asn Gln Val Gln Ser Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Leu Tyr Gln Lys Leu 290 Trp Cys Thr Ser Ser Gln Met Ile Gly Asn Gln Val Gln Cys Cys Thr Cys Leu 295 Trp Cys Thr Met Tyr 265 Trp Cys Tyr Gln Lys Leu 290 Trp Cys Thr Cys Tyr Cys Thr Met Tyr 285 Trp Cys Tyr Gln Lys Leu 290 Trp Cys Thr Cys Tyr Tyr Cys Tyr Cys Tyr Tyr Cys Tyr Cys Tyr Cys Tyr Cys Tyr Tyr Tyr Cys Tyr Tyr Tyr Ty

Ser Val Lys Ile Ser Cys Leu 300 305

- (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..378
 - (D) OTHER INFORMATION: /note= "OCIF-CL"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

His Cys Thr Ala Lys Trp Lys Thr ___ Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 130 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg 180 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 225 230 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala 260 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly 275 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn 305 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 320 325 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 355 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser

(2) INFORMATION FOR SEQ ID NO:74:

370

- (i) SEQUE CHARACTERISTICS:
 - (A) GTH: 351 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..330
 - (D) OTHER INFORMATION: /note= "OCIF-CC"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 50 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
- Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
- Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120
- Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135
- Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 150 150
- Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 160 165 170
- Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg 175 180 185
- Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
- Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile 205 210 215
- Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 220 225 230 235

ln Asn Lys Asp Gln Asp Ile Val L ys Ile Ile Gln 245

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His 320 325

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 amino acids
 - (B) TYPE: amino acid

 - (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..251
 - (D) OTHER INFORMATION: /note= "OCIF-CDD2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Asn Asn Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 85

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg

Cys Pro As Day Phe Phe Ser Asn Glu Thr Ser Se s Ala Pro Cys 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg 175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val 190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
240 245 250

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..176
 - (D) OTHER INFORMATION: /note= "OCIF-CDD1"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp -5 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Thr Gln Lys 140 145 150 150

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr 160 165 170

Gln Lys Cys Gly Ile 175

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: /note= "OCIF-CCR4"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..85
 - (D) OTHER INFORMATION: /note= "OCIF-CCR3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu 80 85
- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..372
 - (D) OTHER INFORMATION: /note= "OCIF-CBst"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Leu Cys Cys Ala Leu Val Phe L sp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 130 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 150 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg 180 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val 195 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 325

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 350 355 360

Phe Leu Glu Met Ile Gly Asn Leu Val 365 370

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..300
 - (D) OTHER INFORMATION: /note= "OCIF-CSph"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
 - Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 - Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 - Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
 - Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
 - Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 55
 - Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 70 75
 - Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr 80 85 90
 - Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe 95 100 105
 - Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 - Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135
 - Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 150 150
 - Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
 - Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile 205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu 220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln 240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala 255 260 265

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly 270 275 280

Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Leu 285 290 295

Asp

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: /note= "OCIF-CBsp"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
- Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
- Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 10
- Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr 15 20 25
- Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro 30 35 40
- Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys 45 55
- Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu 60 65 70 75
- Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr

Y3 .

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg 110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys 125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys 140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly 160 165

- (2) INFORMATION FOR SEQ ID NO:82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: /note= "OCIF-CPst"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro $30 \hspace{1cm} 35 \hspace{1cm} 40$

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 55

Leu Tyr Leu Val

- (2) INFORMATION FOR SEQ ID NO:83:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(ix) FEATU (A) NAME/KEY: -

(B) LOCATION: 1..1206

(D) OTHER INFORMATION: /note= "(OCIF-C19S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AAAGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

(xi) SE	SQUENC	RIPTION: SI	EQ ID NO:84:			
ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGAGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
ממימיי						1206

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C21S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
тстсасааат	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180

GTGTGCGCCC	CTTG	CCACTACTAC	ACAGACAGCT	GGCACAC	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCAG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
AATATT						1206

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -

 - (B) LOCATION: 1..1206
 (D) OTHER INFORMATION: /note= "(OCIF-C22S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360

CATAGGAGCT GC	TTGGAGTG	GTGCAAGCTG	GAACCO	GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TG	GGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA CAAATTGCAG TG	TCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA TATGTTCCGG AA	ACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CA	GGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GC	CTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AG	BAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC AAGATATAGT CA	AGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TG	CTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GG	GAGCAGAA	GACATTGAAA	AAACAATAAA	GGCAAGCAAA	960
CCCAGTGACC AGATCCTGAA GC	TGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CG	CACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA GA	ACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT TATTTTAGA AA	ATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
ТТАТАА					1206

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

 - (A) NAME/KEY: (B) LOCATION: 1..1206
 (D) OTHER INFORMATION: /note= "(OCIF-C23S)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600

CTGTGTGAGG	AGGCA	CAGGTTTGCT	GTTCCTACAA	AGTTTACC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTAGA	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCAGC	1200
AATATT						1206

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1083
 (D) OTHER INFORMATION: /note= "(OCIF-DCR1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

	ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
,	CAGGAACCTT	GCCCTGACCA	CTACTACACA	GACAGCTGGC	ACACCAGTGA	CGAGTGTCTA	120
	TACTGCAGCC	CCGTGTGCAA	GGAGCTGCAG	TACGTCAAGC	AGGAGTGCAA	TCGCACCCAC	180
	AACCGCGTGT	GCGAATGCAA	GGAAGGGCGC	TACCTTGAGA	TAGAGTTCTG	CTTGAAACAT	240
	AGGAGCTGCC	CTCCTGGATT	TGGAGTGGTG	CAAGCTGGAA	CCCCAGAGCG	AAATACAGTT	300
	TGCAAAAGAT	GTCCAGATGG	GTTCTTCTCA	AATGAGACGT	CATCTAAAGC	ACCCTGTAGA	360
	AAACACACAA	ATTGCAGTGT	CTTTGGTCTC	CTGCTAACTC	AGAAAGGAAA	TGCAACACAC	420
	GACAACATAT	GTTCCGGAAA	CAGTGAATCA	ACTCAAAAAT	GTGGAATAGA	TGTTACCCTG	480
	TGTGAGGAGG	CATTCTTCAG	GTTTGCTGTT	CCTACAAAGT	TTACGCCTAA	CTGGCTTAGT	540
	GTCTTGGTAG	ACAATTTGCC	TGGCACCAAA	GTAAACGCAG	AGAGTGTAGA	GAGGATAAAA	600
	CGGCAACACA	GCTCACAAGA	ACAGACTTTC	CAGCTGCTGA	AGTTATGGAA	ACATCAAAAC	660
	AAAGACCAAG	ATATAGTCAA	GAAGATCATC	CAAGATATTG	ACCTCTGTGA	AAACAGCGTG	720
	CAGCGGCACA	TTGGACATGC	TAACCTCACC	TTCGAGCAGC	TTCGTAGCTT	GATGGAAAGC	780

TTACCGGGAA	AGA GCC-	AGCAGAAGAC	ATTGAAAAAA	CAATAA	ATGCAAACCC	840
AGTGACCAGA	TCCTGAAGCT	GCTCAGTTTG	TGGCGAATAA	AAAATGGCGA	CCAAGACACC	900
TTGAAGGGCC	TAATGCACGC	ACTAAAGCAC	TCAAAGACGT	ACCACTTTCC	CAAAACTGTC	960
ACTCAGAGTC	TAAAGAAGAC	CATCAGGTTC	CTTCACAGCT	TCACAATGTA	CAAATTGTAT	1020
CAGAAGTTAT	TTTTAGAAAT	GATAGGTAAC	CAGGTCCAAT	CAGTAAAAAT	AAGCTGCTTA	1080
TAA						1083

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: -(B) LOCATION: 1..1080
 - (D) OTHER INFORMATION: /note= "(OCIF-DCR2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCG	AATGCAAGGA	AGGGCGCTAC	CTTGAGATAG	AGTTCTGCTT	GAAACATAGG	240
AGCTGCCCTC	CTGGATTTGG	AGTGGTGCAA	GCTGGAACCC	CAGAGCGAAA	TACAGTTTGC	300
AAAAGATGTC	CAGATGGGTT	CTTCTCAAAT	GAGACGTCAT	CTAAAGCACC	CTGTAGAAAA	360
CACACAAATT	GCAGTGTCTT	TGGTCTCCTG	CTAACTCAGA	AAGGAAATGC	AACACACGAC	420
AACATATGTT	CCGGAAACAG	TGAATCAACT	CAAAAATGTG	GAATAGATGT	TACCCTGTGT	480
GAGGAGGCAT	TCTTCAGGTT	TGCTGTTCCT	ACAAAGTTTA	CGCCTAACTG	GCTTAGTGTC	540
TTGGTAGACA	ATTTGCCTGG	CACCAAAGTA	AACGCAGAGA	GTGTAGAGAG	GATAAAACGG	600
CAACACAGCT	CACAAGAACA	GACTTTCCAG	CTGCTGAAGT	TATGGAAACA	TCAAAACAAA	660
GACCAAGATA	TAGTCAAGAA	GATCATCCAA	GATATTGACC	TCTGTGAAAA	CAGCGTGCAG	720
CGGCACATTG	GACATGCTAA	CCTCACCTTC	GAGCAGCTTC	GTAGCTTGAT	GGAAAGCTTA	780
CCGGGAAAGA	AAGTGGGAGC	AGAAGACATT	GAAAAAACAA	TAAAGGCATG	CAAACCCAGT	840
GACCAGATCC	TGAAGCTGCT	CAGTTTGTGG	CGAATAAAAA	ATGGCGACCA	AGACACCTTG	900
AAGGGCCTAA	TGCACGCACT	AAAGCACTCA	AAGACGTACC	ACTTTCCCAA	AACTGTCACT	960
CAGAGTCTAA	AGAAGACCAT	CAGGTTCCTT	CACAGCTTCA	CAATGTACAA	ATTGTATCAG	1020
AAGTTATTTT	TAGAAATGAT	AGGTAACCAG	GTCCAATCAG	TAAAAATAAG	CTGCTTATAA	1080

43 ID NO:90: (2) INFORMATION

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1092 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1092
 - (D) OTHER INFORMATION: /note= "(OCIF-DCR3)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCAGATG	TCCAGATGGG	TTCTTCTCAA	ATGAGACGTC	ATCTAAAGCA	360
CCCTGTAGAA	AACACACAAA	TTGCAGTGTC	TTTGGTCTCC	TGCTAACTCA	GAAAGGAAAT	420
GCAACACACG	ACAACATATG	TTCCGGAAAC	AGTGAATCAA	CTCAAAAATG	TGGAATAGAT	480
GTTACCCTGT	GTGAGGAGGC	ATTCTTCAGG	TTTGCTGTTC	CTACAAAGTT	TACGCCTAAC	540
TGGCTTAGTG	TCTTGGTAGA	CAATTTGCCT	GGCACCAAAG	TAAACGCAGA	GAGTGTAGAG	600
AGGATAAAAC	GGCAACACAG	CTCACAAGAA	CAGACTTTCC	AGCTGCTGAA	GTTATGGAAA	660
CATCAAAACA	AAGACCAAGA	TATAGTCAAG	AAGATCATCC	AAGATATTGA	CCTCTGTGAA	720
AACAGCGTGC	AGCGGCACAT	TGGACATGCT	AACCTCACCT	TCGAGCAGCT	TCGTAGCTTG	780
ATGGAAAGCT	TACCGGGAAA	GAAAGTGGGA	GCAGAAGACA	TTGAAAAAAC	AATAAAGGCA	840
TGCAAACCCA	GTGACCAGAT	CCTGAAGCTG	CTCAGTTTGT	GGCGAATAAA	AAATGGCGAC	900
CAAGACACCT	TGAAGGGCCT	AATGCACGCA	CTAAAGCACT	CAAAGACGTA	CCACTTTCCC	960
AAAACTGTCA	CTCAGAGTCT	AAAGAAGACC	ATCAGGTTCC	TTCACAGCTT	CACAATGTAC	1020
AAATTGTATC	AGAAGTTATT	TTTAGAAATG	ATAGGTAACC	AGGTCCAATC	AGTAAAAATA	1080
AGCTGCTTAT	AA					1092

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(ix) FEATU (A) 1 (B) LOCATION: 1..1080 (D) OTHER INFORMATION: /note= "(OCIF-DCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240 300 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA 420 GTTTGCAAAT CCGGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCCTGTGT 480 GAGGAGGCAT TCTTCAGGTT TGCTGTTCCT ACAAAGTTTA CGCCTAACTG GCTTAGTGTC 540 TTGGTAGACA ATTTGCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAAACGG 600 CAACACAGCT CACAAGAACA GACTTTCCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA 660 GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTGAAAA CAGCGTGCAG 720 CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA 780 CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAACAA TAAAGGCATG CAAACCCAGT 840 GACCAGATCC TGAAGCTGCT CAGTTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG 900 AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT 960 CAGAGTCTAA AGAAGACCAT CAGGTTCCTT CACAGCTTCA CAATGTACAA ATTGTATCAG 1020 AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA 1080

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 981 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..981
 - (D) OTHER INFORMATION: /note= "(OCIF-DDD1)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120

TGTGACAAAT	GTC T66	TACCTACCTA	AAACAACACT	GTACAG	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATATTGAC	600
CTCTGTGAAA	ACAGCGTGCA	GCGGCACATT	GGACATGCTA	ACCTCACCTT	CGAGCAGCTT	660
CGTAGCTTGA	TGGAAAGCTT	ACCGGGAAAG	AAAGTGGGAG	CAGAAGACAT	TGAAAAAACA	720
ATAAAGGCAT	GCAAACCCAG	TGACCAGATC	CTGAAGCTGC	TCAGTTTGTG	GCGAATAAAA	780
AATGGCGACC	AAGACACCTT	GAAGGGCCTA	ATGCACGCAC	TAAAGCACTC	AAAGACGTAC	840
CACTTTCCCA	AAACTGTCAC	TCAGAGTCTA	AAGAAGACCA	TCAGGTTCCT	TCACAGCTTC	900
ACAATGTACA	AATTGTATCA	GAAGTTATTT	TTAGAAATGA	TAGGTAACCA	GGTCCAATCA	960
GTAAAAATAA	GCTGCTTATA	A				981

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 984 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..984
 - (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600

CTGTGTGAGG	AGGCA	CAGGTTTGCT	GTTCCTACAA	AGTTTAC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGACG	CACTAAAGCA	CTCAAAGACG	840
TACCACTTTC	CCAAAACTGT	CACTCAGAGT	CTAAAGAAGA	CCATCAGGTT	CCTTCACAGC	900
TTCACAATGT	ACAAATTGTA	TCAGAAGTTA	TTTTTAGAAA	TGATAGGTAA	CCAGGTCCAA	960
TCAGTAAAAA	TAAGCTGCTT	ATAA				984

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1200 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "(OCIF-CL)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020

ACCTTGAAGG GCCTI CA CGCACTAAAG CACTCAAAGA CGTACCAC TCCCAAAACT 1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAA GTACAAATTG 1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA 1200

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1056 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1056
 - (D) OTHER INFORMATION: /note= "(OCIF-CC)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGAACAACT TGCTGTGCT	G CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT TTCCTCCAA	A GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTG	G TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTG	A CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA GCCCCGTGT	G CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG TGTGCGAAT	G CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTG	G ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA GATGTCCAG	A TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA CAAATTGCA	G TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA TATGTTCCC	g aaacagtgaa	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG AGGCATTCT	T CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG TAGACAATT	T GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC ACAGCTCAC	A AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC AAGATATAG	T CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC ACATTGGAC	A TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG GAAAGAAA	T GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC AGATCCTGA	A GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGO	A CGCACTAAAG	CACTGA			1056

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

ριγ: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..819

(D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGAACAACT TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	. 120
TGTGACAAAT GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC AAGATATAGT	CAAGAAGATC	ATCCAATGA			819

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -(B) LOCATION: 1..594
- (D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120 180 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACAT GTACAGCAAA GTGGAAGACC GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240

CTATACTGCA GCCO GT& CAAGGAGCTG CAGTACGTCA AGCAGGA CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT ATGA	594
(2) INFORMATION FOR SEQ ID NO:98:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 432 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
<pre>(ix) FEATURE: (A) NAME/KEY: - (B) LOCATION: 1432 (D) OTHER INFORMATION: /note= "(OCIF-CCR4)"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAGA GCGAAATACA	420
GTTTGCAAAT GA	432
(2) INFORMATION FOR SEQ ID NO:99:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: (B) LOCATION: 1..321
 (D) OTHER INFORMATION: /note= "(OCIF-CCR3)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99: ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60

CAGGAAACGT	TTCC	GTACCTTCAT	TATGACGAAG	ÄAACCTC	TCAGCTGTTG	120
rgtgacaaat	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCALL	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	A				321

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1182
 - (D) OTHER INFORMATION: /note= "(OCIF-CBst)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCACTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCTAGTCT	AG		1182

- (2) INFORMATION SEQ ID NO:101:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..966
 - (D) OTHER INFORMATION: /note= "(OCIF-CSph)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCCTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCTAGTCTA	960
GACTAG						966

- (2) INFORMATION FOR SEQ ID NO:102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 564 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - ,..,
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..564

(D)	sh formation:	/note=	"(OCIF-CBsp	

(xi)	SEOUENCE	DESCRIPTION:	SEQ	ID	NO:102:
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ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC		60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG		120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC		180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	;	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC		300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	بد	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	*	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCTGT		480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA		540
CACGACAACA	TATGTTCCGG	CTAG					564

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /note= "(OCIF-Pst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC 60 CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240 CTATACCTAG TCTAG 255

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1317 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1317

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(D)

(ix) FEATURE:

(A) NAME/KEY: sig_peptide (B) LOCATION: 1173..1202

(D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAGACAT	ATAACTTGAA	CACTTGGCCC	TGATGGGGAA	GCAGCTCTGC	AGGGACTTTT	60
TCAGCCATCT	GTAAACAATT	TCAGTGGCAA	CCCGCGAACT	GTAATCCATG	AATGGGACCA	120
CACTTTACAA	GTCATCAAGT	CTAACTTCTA	GACCAGGGAA	TTAATGGGGG	AGACAGCGAA	180
CCCTAGAGCA	AAGTGCCAAA	CTTCTGTCGA	TAGCTTGAGG	CTAGTGGAAA	GACCTCGAGG	240
AGGCTACTCC	AGAAGTTCAG	CGCGTAGGAA	GCTCCGATAC	CAATAGCCCT	TTGATGATGG	300
TGGGGTTGGT	GAAGGGAACA	GTGCTCCGCA	AGGTTATCCC	TGCCCCAGGC	AGTCCAATTT	360
TCACTCTGCA	GATTCTCTCT	GGCTCTAACT	ACCCCAGATA	ACAAGGAGTG	AATGCAGAAT	420
AGCACGGGCT	TTAGGGCCAA	TCAGACATTA	GTTAGAAAAA	TTCCTACTAC	ATGGTTTATG	480
TAAACTTGAA	GATGAATGAT	TGCGAACTCC	CCGAAAAGGG	CTCAGACAAT	GCCATGCATA	540
AAGAGGGGCC	CTGTAATTTG	AGGTTTCAGA	ACCCGAAGTG	AAGGGGTCAG	GCAGCCGGGT	600
ACGGCGGAAA	CTCACAGCTT	TCGCCCAGCG	AGAGGACAAA	GGTCTGGGAC	ACACTCCAAC	660
TGCGTCCGGA	TCTTGGCTGG	ATCGGACTCT	CAGGGTGGAG	GAGACACAAG	CACAGCAGCT	720
GCCCAGCGTG	TGCCCAGCCC	TCCCACCGCT	GGTCCCGGCT	GCCAGGAGGC	TGGCCGCTGG	780
CGGGAAGGGG	CCGGGAAACC	TCAGAGCCCC	GCGGAGACAG	CAGCCGCCTT	GTTCCTCAGC	840
CCGGTGGCTT	TTTTTTCCCC	TGCTCTCCCA	GGGGACAGAC	ACCACCGCCC	CACCCCTCAC	900
GCCCCACCTC	CCTGGGGGAT	CCTTTCCGCC	CCAGCCCTGA	AAGCGTTAAT	CCTGGAGCTT	960
TCTGCACACC	CCCCGACCGC	TCCCGCCCAA	GCTTCCTAAA	AAAGAAAGGT	GCAAAGTTTG	1020
GTCCAGGATA	GAAAAATGAC	TGATCAAAGG	CAGGCGATAC	TTCCTGTTGC	CGGGACGCTA	1080
TATATAACGT	GATGAGCGCA	CGGGCTGCGG	AGACGCACCG	GAGCGCTCGC	CCAGCCGCCG	1140
CCTCCAAGCC	CCTGAGGTTT	CCGGGGACCA	CAATGAACAA	GTTGCTGTGC	TGCGCGCTCG	1200
TGGTAAGTCC	CTGGGCCAGC	CGACGGGTGC	CCGGCGCCTG	GGGAGGCTGC	TGCCACCTGG	1260
TCTCCCAACC	TCCCAGCGGA	CCGGCGGGGA	AAAAGGCTCC	ACTCGCTCCC	TCCCAAG	1317

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10190 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 130..162

(D) CR LAFORMATION: /note= "amino aci sidues -11 to -1"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(130..162, 163..498, 4503..4694, 6715..6939, 8960..9346)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(163..498, 4503..4694, 6715..6939, 8960..9346)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:								
GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT 60								
ACTGTTGCAC ATAAGAACAA ACCTATTTC ATGCTAAGAT GATGCCACTG TGTTCCTTTC	120							
TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr -11 -10 -5 1	168							
TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu 5 10 15	216							
TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr 20 25 30	264							
GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr 35 40 45 50	312							
GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys 55 60 65	360							
AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg 70 75 80	408							
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu 85 90 95	456							
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala 100 105 110	498							
GGTACGTGTC AATGTGCAGC AAAATTAATT AGGATCATGC AAAGTCAGAT AGTTGTGACA	558							
GTTTAGGAGA ACACTTTTGT TCTGATGACA TTATAGGATA GCAAATTGCA AAGGTAATGA	618							
AACCTGCCAG GTAGGTACTA TGTGTCTGGA GTGCTTCCAA AGGACCATTG CTCAGAGGAA	678							
TACTTTGCCA CTACAGGGCA ATTTAATGAC AAATCTCAAA TGCAGCAAAT TATTCTCTCA	738							
TGAGATGCAT GATGGTTTTT TTTTTTTTT TTAAAGAAAC AAACTCAAGT TGCACTATTG	798							
ATAGTTGATC TATACCTCTA TATTTCACTT CAGCATGGAC ACCTTCAAAC TGCAGCACTT	858							
TTTGACAAAC ATCAGAAATG TTAATTTATA CCAAGAGAGT AATTATGCTC ATATTAATGA	918							
GACTCTGGAG TGCTAACAAT AAGCAGTTAT AATTAATTAT GTAAAAAATG AGAATGGTGA	978							
GGGGAATTGC ATTTCATTAT TAAAAACAAG GCTAGTTCTT CCTTTAGCAT GGGAGCTGAG	1038							

TGTTTGGGAG GGT	ATAGCAGAAT	CTCTTCAATG	AGCTTAT	TIATCTTAGA	1098
CAAAACAGAT TGTCGCCA	AGAGCAAGCA	CTTGCCTATA	AACCAAC	TTTCTCTTTT	1158
GCATTTTGAA CAGCATTGGT	CAGGGCTCAT	GTGTATTGAA	TCTTTTAAAC	CAGTAACCCA	1218
CGTTTTTTT CTGCCACATT	TGCGAAGCTT	CAGTGCAGCC	TATAACTTTT	CATAGCTTGA	1278
GAAAATTAAG AGTATCCACT	TACTTAGATG	GAAGAAGTAA	TCAGTATAGA	TTCTGATGAC	1338
TCAGTTTGAA GCAGTGTTTC	TCAACTGAAG	CCCTGCTGAT	ATTTTAAGAA	ATATCTGGAT	1398
TCCTAGGCTG GACTCCTTTT	TGTGGGCAGC	TGTCCTGCGC	ATTGTAGAAT	TTTGGCAGCA	1458
CCCCTGGACT CTAGCCACTA	GATACCAATA	GCAGTCCTTC	CCCCATGTGA	CAGCCAAAAA	1518
TGTCTTCAGA CACTGTCAAA	TGTCGCCAGG	TGGCAAAATC	ACTCCTGGTT	GAGAACAGGG	1578
TCATCAATGC TAAGTATCTG	TAACTATTTT	AACTCTCAAA	ACTTGTGATA	TACAAAGTCT	1638
AAATTATTAG ACGACCAATA	CTTTAGGTTT	AAAGGCATAC	AAATGAAACA	TTCAAAAATC	1698
AAAATCTATT CTGTTTCTCA	AATAGTGAAT	CTTATAAAAT	TAATCACAGA	AGATGCAAAT	1758
TGCATCAGAG TCCCTTAAAA	TTCCTCTTCG	TATGAGTATT	TGAGGGAGGA	ATTGGTGATA	1818
GTTCCTACTT TCTATTGGAT	GGTACTTTGA	GACTCAAAAG	CTAAGCTAAG	TTGTGTGTGT	1878
GTCAGGGTGC GGGGTGTGGA	ATCCCATCAG	ATAAAAGCAA	ATCCATGTAA	TTCATTCAGT	1938
AAGTTGTATA TGTAGAAAAA	TGAAAAGTGG	GCTATGCAGC	TTGGAAACTA	GAGAATTTTG	1998
AAAAATAATG GAAATCACAA	GGATCTTTCT	TAAATAAGTA	AGAAAATCTG	TTTGTAGAAT	2058
GAAGCAAGCA GGCAGCCAGA	AGACTCAGAA	CAAAAGTACA	CATTTTACTC	TGTGTACACT	2118
GGCAGCACAG TGGGATTTAT	TTACCTCTCC	CTCCCTAAAA	ACCCACACAG	CGGTTCCTCT	2178
TGGGAAATAA GAGGTTTCCA	GCCCAAAGAG	AAGGAAAGAC	TATGTGGTGT	TACTCTAAAA	2238
AGTATTTAAT AACCGTTTTG	TTGTTGCTGT	TGCTGTTTTG	AAATCAGATT	GTCTCCTCTC	2298
CATATTTTAT TTACTTCATT	CTGTTAATTC	CTGTGGAATT	ACTTAGAGCA	AGCATGGTGA	2358
ATTCTCAACT GTAAAGCCAA	ATTTCTCCAT	CATTATAATT	TCACATTTTG	CCTGGCAGGT	2418
TATAATTTTT ATATTTCCAC	TGATAGTAAT	AAGGTAAAAT	CATTACTTAG	ATGGATAGAT	2478
CTTTTTCATA AAAAGTACCA	TCAGTTATAG	AGGGAAGTCA	TGTTCATGTT	CAGGAAGGTC	2538
ATTAGATAAA GCTTCTGAAT	ATATTATGAA	ACATTAGTTC	TGTCATTCTT	AGATTCTTTT	2598
TGTTAAATAA CTTTAAAAGC	TAACTTACCT	AAAAGAAATA	TCTGACACAT	ATGAACTTCT	2658
CATTAGGATG CAGGAGAAGA	CCCAAGCCAC	AGATATGTAT	CTGAAGAATG	AACAAGATTC	2718
TTAGGCCCGG CACGGTGGCT	CACATCTGTA	ATCTCAAGAG	TTTGAGAGGT	CAAGGCGGGC	2778
AGATCACCTG AGGTCAGGAG	TTCAAGACCA	GCCTGGCCAA	CATGATGAAA	CCCTGCCTCT	2838
ACTAAAAATA CAAAAATTAG	CAGGGCATGG	TGGTGCATGC	CTGCAACCCT	AGCTACTCAG	2898
GAGGCTGAGA CAGGAGAATC	TCTTGAACCC	TCGAGGCGGA	GGTTGTGGTG	AGCTGAGATC	2958
CCTCTACTGC ACTCCAGCCT	GGGTGACAGA	GATGAGACTC	CGTCCCTGCC	GCCGCCCCG	3018
CCTTCCCCCC CAAAAAGATT	CTTCTTCATG	CAGAACATAC	GGCAGTCAAC	AAAGGGAGAC	3078

A B A B B B B B B B B B B	
CTGGGTCCAG GTGT AGI CACTTATTTC GAGTAAATTA GCAATGA	3138
AATCCCTGCC CAAATACCTC TGCTTATGAT ATTGTAGAAT TTGATATAGA GTTGTATCCC	3198
ATTTAAGGAG TAGGATGTAG TAGGAAAGTA CTAAAAACAA ACACACAAAC AGAAAACCCT	3258
CTTTGCTTTG TAAGGTGGTT CCTAAGATAA TGTCAGTGCA ATGCTGGAAA TAATATTTAA	3318
TATGTGAAGG TTTTAGGCTG TGTTTTCCCC TCCTGTTCTT TTTTTCTGCC AGCCCTTTGT	3378
CATTTTTGCA GGTCAATGAA TCATGTAGAA AGAGACAGGA GATGAAACTA GAACCAGTCC	3438
ATTTTGCCCC TTTTTTATT TTCTGGTTTT GGTAAAAGAT ACAATGAGGT AGGAGGTTGA	3498
GATTTATAAA TGAAGTTTAA TAAGTTTCTG TAGCTTTGAT TTTTCTCTTT CATATTTGTT	3558
ATCTTGCATA AGCCAGAATT GGCCTGTAAA ATCTACATAT GGATATTGAA GTCTAAATCT	3618
GTTCAACTAG CTTACACTAG ATGGAGATAT TTTCATATTC AGATACACTG GAATGTATGA	3678
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TTGTGGACTG GTTCAAGTTT TTCTGCCAAT GATTTCTTCA AATTTATCAA ATATTTTTCC	3798
ATCATGAAGT AAAATGCCCT TGCAGTCACC CTTCCTGAAG TTTGAACGAC TCTGCTGTTT	3858
TAAACAGTTT AAGCAAATGG TATATCATCT TCCGTTTACT ATGTAGCTTA ACTGCAGGCT	3918
TACGCTTTTG AGTCAGCGGC CAACTTTATT GCCACCTTCA AAAGTTTATT ATAATGTTGT	3978
AAATTTTTAC TTCTCAAGGT TAGCATACTT AGGAGTTGCT TCACAATTAG GATTCAGGAA	4038
AGAAAGAACT TCAGTAGGAA CTGATTGGAA TTTAATGATG CAGCATTCAA TGGGTACTAA	4098
TTTCAAAGAA TGATATTACA GCAGACACAC AGCAGTTATC TTGATTTTCT AGGAATAATT	4158
GTATGAAGAA TATGGCTGAC AACACGGCCT TACTGCCACT CAGCGGAGGC TGGACTAATG	4218
AACACCCTAC CCTTCTTTCC TTTCCTCTCA CATTTCATGA GCGTTTTGTA GGTAACGAGA	4278
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TTTTGTTCTG TCTAATGAAG TGAAAAATGA AAATGCTAGA GTTTTGTGCA ACATAATAGT	4398
AGCAGTAAAA ACCAAGTGAA AAGTCTTTCC AAAACTGTGT TAAGAGGGCA TCTGCTGGGA	4458
AACGATTTGA GGAGAAGGTA CTAAATTGCT TGGTATTTTC CGTA GGA ACC CCA GAG Gly Thr Pro Glu 115	4514
CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu 120 125 130	4562
ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe 135 140 145	4610
GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT Gly Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys 150 160	4658
TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT GGA ATA GGTAATTACA Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile 165 170 175	4704
	450

TTCCAAAATA CGTCTTTGTA CGATTTTGTA GTATCATCTC TCTCTCTGAG TTGAACACAA 4764

GGCCTCCAG	C CACITATIO	G TCAAACTTA	CATTTTCCCT	TTCTTG	TTAACCAGCT	4824
AAGGCTACT	C TCGATGCATT	ACTGCTAAAG	CTACCACTCA	GAATCTC	AAAACTCATC	4884
TTCTCACAG	A TAACACCTCA	AAGCTTGATT	TTCTCTCCTT	TCACACTGAA	ATCAAATCTT	4944
GCCCATAGG	C AAAGGGCAGT	GTCAAGTTTG	CCACTGAGAT	GAAATTAGGA	GAGTCCAAAC	5004
TGTAGAATT	C ACGTTGTGTG	TTATTACTTT	CACGAATGTC	TGTATTATTA	ACTAAAGTAT	5064
ATATTGGCA	A CTAAGAAGCA	AAGTGATATA	AACATGATGA	CAAATTAGGC	CAGGCATGGT	5124
GGCTTACTC	C TATAATCCCA	ACATTTTGGG	GGGCCAAGGT	AGGCAGATCA	CTTGAGGTCA	5184
GGATTTCAA	G ACCAGCCTGA	CCAACATGGT	GAAACCTTGT	CTCTACTAAA	AATACAAAAA	5244
TTAGCTGGG	C ATGGTAGCAG	GCACTTCTAG	TACCAGCTAC	TCAGGGCTGA	GGCAGGAGAA	5304
TCGCTTGAA	C CCAGGAGATG	GAGGTTGCAG	TGAGCTGAGA	TTGTACCACT	GCACTCCAGT	5364
CTGGGCAAC	A GAGCAAGATT	TCATCACACA	CACACACACA	CACACACACA	CACACATTAG	5424
AAATGTGTA	C TTGGCTTTGT	TACCTATGGT	ATTAGTGCAT	CTATTGCATG	GAACTTCCAA	5484
GCTACTCTG	g TTGTGTTAA G	CTCTTCATTG	GGTACAGGTC	ACTAGTATTA	AGTTCAGGTT	5544
ATTCGGATG	C ATTCCACGGT	AGTGATGACA	ATTCATCAGG	CTAGTGTGTG	TGTTCACCTT	5604
GTCACTCCC	A CCACTAGACT	AATCTCAGAC	CTTCACTCAA	AGACACATTA	CACTAAAGAT	5664
GATTTGCTT	T TTTGTGTTTA	ATCAAGCAAT	GGTATAAACC	AGCTTGACTC	TCCCCAAACA	5724
GTTTTTCGT	A CTACAAAGAA	GTTTATGAAG	CAGAGAAATG	TGAATTGATA	TATATATGAG	5784
ATTCTAACC	C AGTTCCAGCA	TTGTTTCATT	GTGTAATTGA	AATCATAGAC	AAGCCATTTT	5844
AGCCTTTGC	T TTCTTATCTA	ААААААААА	AAAAAAAATG	AAGGAAGGGG	TATTAAAAGG	5904
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TATTGTGCA	C TTACTATGTG	GTACTGTGCT	ATAGAGGCTT	TAACATTTAT	AAAAACACTG	6024
TGAAAGTTG	C TTCAGATGAA	TATAGGTAGT	AGAACGGCAG	AACTAGTATT	CAAAGCCAGG	6084
TCTGATGAA	т ссааааасаа	ACACCCATTA	CTCCCATTTT	CTGGGACATA	CTTACTCTAC	6144
CCAGATGCT	C TGGGCTTTGT	AATGCCTATG	TAAATAACAT	AGTTTTATGT	TTGGTTATTT	6204
TCCTATGTA	A TGTCTACTTA	TATATCTGTA	TCTATCTCTT	GCTTTGTTTC	CAAAGGTAAA	6264
CTATGTGTC	T AAATGTGGGC	AAAAAATAAC	ACACTATTCC	AAATTACTGT	TCAAATTCCT	6324
TTAAGTCAG	T GATAATTATT	TGTTTTGACA	TTAATCATGA	AGTTCCCTGT	GGGTACTAGG	6384
TAAACCTTT	A ATAGAATGTT	AATGTTTGTA	TTCATTATAA	GAATTTTTGG	CTGTTACTTA	6444
TTTACAACA	A TATTTCACTC	TAATTAGACA	TTTACTAAAC	TTTCTCTTGA	AAACAATGCC	6504
CAAAAAAGA	A CATTAGAAGA	CACGTAAGCT	CAGTTGGTCT	CTGCCACTAA	GACCAGCCAA	6564
CAGAAGCTT	G ATTTTATTCA	AACTTTGCAT	TTTAGCATAT	TTTATCTTGG	AAAATTCAAT	6624
TGTGTTGGT	T TTTTGTTTT	GTTTGTATTG	AATAGACTCT	CAGAAATCCA	ATTGTTGAGT	6684
AAATCTTCT	G GGTTTTCTAA	CCTTTCTTTA		C CTG TGT G r Leu Cys G 180		6738

TTC TTC AGG TTT GTT CCT ACA AAG TTT ACG CCT AAC CCT AGT Phe Phe Arg Ph	6786
GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val 205 210 215	6834
GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu 220 225 230	6882
CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys 235 240 245	6930
ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTTGTA CGATTTTGTA Ile Ile Gln 250	6979
GTATCATCTC TCTCTCTGAG TTGAACACAA GGCCTCCAGC CACATTCTTG GTCAAACTTA	7039
CATTTTCCCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG	7099
CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT	7159
TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTTG	7219
CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGTAGAATTC ACGTTGTGTG TTATTACTTT	7279
CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAAGCA AAGTGATATA	7339
AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTTGGG	7399
GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTTCAAG ACCAGCCTGA CCAACATGGT	7459
GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG	7519
TACCAGCTAC TCAGGGCTGA GGCAGGAGAA TCGCTTGAAC CCAGGAGATG GAGGTTGCAG	7579
TGAGCTGAGA TTGTACCACT GCACTCCAGT CTGGGCAACA GAGCAAGATT TCATCACACA	7639
CACACACAC CACACACACA CACACATTAG AAATGTGTAC TTGGCTTTGT TACCTATGGT	7699
ATTAGTGCAT CTATTGCATG GAACTTCCAA GCTACTCTGG TTGTGTTAAG CTCTTCATTG	7759
GGTACAGGTC ACTAGTATTA AGTTCAGGTT ATTCGGATGC ATTCCACGGT AGTGATGACA	7819
ATTCATCAGG CTAGTGTGTG TGTTCACCTT GTCACTCCCA CCACTAGACT AATCTCAGAC	7879
CTTCACTCAA AGACACATTA CACTAAAGAT GATTTGCTTT TTTGTGTTTA ATCAAGCAAT	7939
GGTATAAACC AGCTTGACTC TCCCCAAACA GTTTTTCGTA CTACAAAGAA GTTTATGAAG	7999
CAGAGAAATG TGAATTGATA TATATATGAG ATTCTAACCC AGTTCCAGCA TTGTTTCATT	8059
GTGTAATTGA AATCATAGAC AAGCCATTTT AGCCTTTGCT TTCTTATCTA AAAAAAAAAA	8119
AAAAAAAATG AAGGAAGGGG TATTAAAAGG AGTGATCAAA TTTTAACATT CTCTTTAATT	8179
AATTCATTTT TAATTTTACT TTTTTTCATT TATTGTGCAC TTACTATGTG GTACTGTGCT	8239
ATAGAGGCTT TAACATTTAT AAAAACACTG TGAAAGTTGC TTCAGATGAA TATAGGTAGT	8299
AGAACGGCAG AACTAGTATT CAAAGCCAGG TCTGATGAAT CCAAAAACAA ACACCCATTA	8359
CTCCCATTTT CTGGGACATA CTTACTCTAC CCAGATGCTC TGGGCTTTGT AATGCCTATG	8419

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															ATAAC	8539
ACAC	CTAT	rcc i	TAAA	PACTO	T TO	CAAA	rtcci	TT	AAGTO	CAGT	GATA	ATTA	ATT 1	rgtti	TGACA	8599
TTAI	ATCAT	rga i	AGTTO	CCTC	T GO	GTAC	TAGO	TA	AACCI	ATTT	ATAC	TAAE	STT A	AATGI	TTGTA	8659
TTC	ATTAT	CAA (GAATI	TTT	G C	GTT	CTT	A TTT	racai	ACAA	TAT	CACT	CTC :	TAAT	TAGACA	8719
TTTI	ACTA	AAC :	TTTCI	CTTC	A A	ACA	ATGCC	CAA	LAAA	AGAA	CATT	raga <i>i</i>	AGA (CACGI	CAAGCT	8779
CAGI	rtggi	CT (CTGC	CACTA	A G	ACCAC	CCAF	CAC	BAAGO	CTTG	ATT	TAT	rca i	AACTI	TGCAT	8839
TTT	AGCAT	TAT	TTTAT	CTTC	G A	AATT	CAAT	TGI	CTTO	GTT	TTTT	rg tt 1	rtt (GTTTC	TATTG	8899
AATA	AGACT	rct (CAGAI	AATCO	A A	TGT	rgagi	LAA 1	ATCTT	rctg	GGT	TTC	CAA (CCTT	CTTTA	8959
GAT Asp	ATT Ile	GAC Asp	CTC Leu 255	TGT Cys	GAA Glu	AAC Asn	AGC Ser	GTG Val 260	CAG Gln	CGG Arg	CAC His	ATT Ile	GGA Gly 265	CAT His	GCT Ala	9007
AAC Asn	CTC Leu	ACC Thr 270	TTC Phe	GAG Glu	CAG Gln	CTT Leu	CGT Arg 275	AGC Ser	TTG Leu	ATG Met	GAA Glu	AGC Ser 280	TTA Leu	CCG Pro	GGA Gly	9055
AAG Lys	AAA Lys 285	GTG Val	GGA Gly	GCA Ala	GAA Glu	GAC Asp 290	ATT Ile	GAA Glu	AAA Lys	ACA Thr	ATA Ile 295	AAG Lys	GCA Ala	TGC Cys	AAA Lys	9103
CCC Pro 300	AGT Ser	GAC Asp	CAG Gln	ATC Ile	CTG Leu 305	AAG Lys	CTG Leu	CTC Leu	AGT Ser	TTG Leu 310	TGG Trp	CGA Arg	ATA Ile	AAA Lys	AAT Asn 315	9151
GGC Gly	GAC Asp	CAA Gln	GAC Asp	ACC Thr 320	TTG Leu	AAG Lys	GGC Gly	CTA Leu	ATG Met 325	CAC His	GCA Ala	CTA Leu	AAG Lys	CAC His 330	TCA Ser	9199
AAG Lys	ACG Thr	TAC Tyr	CAC His 335	TTT Phe	CCC Pro	AAA Lys	ACT Thr	GTC Val 340	ACT Thr	CAG Gln	AGT Ser	CTA Leu	AAG Lys 345	AAG Lys	ACC Thr	9247
ATC Ile	AGG Arg	TTC Phe 350	CTT Leu	CAC His	AGC Ser	TTC Phe	ACA Thr 355	ATG Met	TAC Tyr	AAA Lys	TTG Leu	TAT Tyr 360	CAG Gln	AAG Lys	TTA Leu	9295
Phe	Leu	Glu	ATG Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	ATA Ile	AGC Ser	TGC Cys	9343
TTA Leu 380	TAA	CTGG.	AAA :	rggc(CATTO	GA G	CTGT	rtcc:	r ca	CAAT'	rggc	GAG	ATCC	CAT		9396
GGA!	rgagʻ	TAA .	ACTG:	TTTC:	rc a	GGCA(CTTG	A GG	CTTT(CAGT	GAT	ATCT	TTC	TCAT	FACCAG	9456
TGA	CTAA'	TTT	TGCC	ACAG	G T	ACTA	AAAG	AA A	CTAT	GATG	TGG	AGAA	AGG .	ACTA	ACATCT	9516
CCT	CCAA	TAA	ACCC	CAAA'	rg g	TTAA'	rcca:	A CT	GTCA	GATC	TGG	ATCG'	TTA	TCTA	CTGACT	9576
ATA	TTTT	ccc	TTAT	TACT	GC T	TGCA	GTAA'	r TC	AACT	GGAA	ATT	AAAA	AAA .	AAAA	ACTAGA	9636
CTC	CACT	GGG	CCTT	ACTA	AA T	ATGG	GAAT	G TC	TAAC'	TTAA	ATA	GCTT	TGG	GATT	CCAGCT	9696
ATG	CTAG.	AGG	CTTT	TATT	AG A	AAGC	CATA	r tt	TTTT	CTGT	AAA	AGTT.	ACT	AATA'	TATCT G	9756
TAA	CACT.	ATT	ACAG'	TATT	GC T	ATTT.	TATA	r ca	TTCA	GATA	TAA	GATT	TGG	ACAT	ATTATC	9816

ATCCTATAAA	GAALTAT	G ACTTAATTT	TAGAAAGAAA	ATTATA	C TTTATTATG	9876
ACAAATGAAA	GAGA-AATAT	ATATTTTTAA	TGGAAAGTTT	GTAGCATf	TCTAATAGGT	9936
ACTGCCATAT	TTTTCTGTGT	GGAGTATTTT	TATAATTTTA	TCTGTATAAG	CTGTAATATC	9996
ATTTTATAGA	AAATGCATTA	TTTAGTCAAT	TGTTTAATGT	TGGAAAACAT	ATGAAATATA	10056
AATTATCTGA	ATATTAGATG	CTCTGAGAAA	TTGAATGTAC	CTTATTTAAA	AGATTTTATG	10116
GTTTTATAAC	TATATAAATG	ACATTATTAA	AGTTTTCAAA	TTATTTTTTA	TTGCTTTCTC	10176
TGTTGCTTTT	ATTT					10190

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro -11 -10 -5 5

Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp

Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp 25 30 35

Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp
40 45 50

His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu 55 60 65

Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu 70 75 80 85

Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His Arg

Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro Glu Arg 105 110 115

Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr 120 125 130

Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe Gly 135 140 145

Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn Ile Cys Ser

Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val Thr Leu Cys

Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn

Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala 200 205 210

Glu Ser Val Glu 3 11e Lys Arg Gln His Ser Ser Gln thr 220 Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile 240 Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser 300 Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met 320 His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr 350 Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu

375 380

- (2) INFORMATION FOR SEQ ID NO:107:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..20
 - (D) OTHER INFORMATION: /note= "synthetic DNA (primer 2F)"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

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- (2) INFORMATION FOR SEQ ID NO:108:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

The second desirence properties and decrease and